

Shown is the 3'UTR of the human IL1B sequence from accession number M15330.

\* Represents the stop codon.

\*AGAGAGCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAG  
GGCTGGCAGAAAGGGAACAGAAAGGTTTTTGTGAGTACGGCTATAGCCTGGAC  
TTTCCTGTTGTCTACACCAATGCCCAACTGCCCTGCCCTAGGGTAGTGCTAA  
GAGGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCC  
AATCCCAGCCCTTTTGTGAGCCAGGCCCTCTCTCACCTCTCCTACTCACT  
TAAAGCCCGCTGACAGAAACCAACGGCCACATTTGGTTCTAAGAAACCCCTC  
TGTCATTGCTCCACATCTGATGAGCAACCGCTTCCCTATTTATTTATT  
TAATTTGTTTGTGTTTATTCATTGGTCTAAATTTATTTCAAAGGGGGCAAG  
AAGTAGCAGTGTCTGTAAAGAGCCCTAGTTTTTAATAGCTATGGAATCAAT  
TCAATTGGACTGGTGTGCTCTCTTTAAATCAAGTCCTTTAATTAAGACTG  
AAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATGAGCAAA  
TATCATACTGTTCAATGGTTCTGAAATAAACTTCTCTGAAG

FIGURE 1

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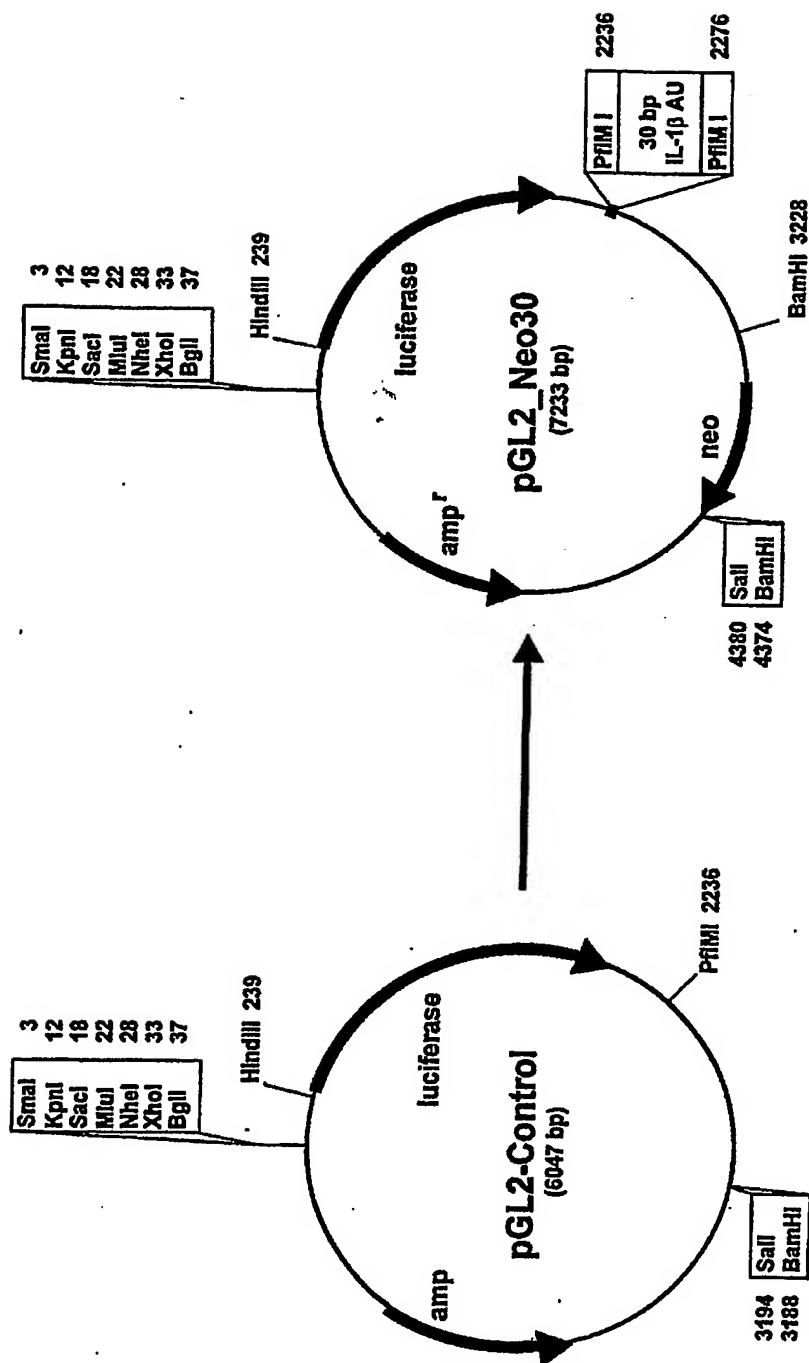


FIGURE 3A

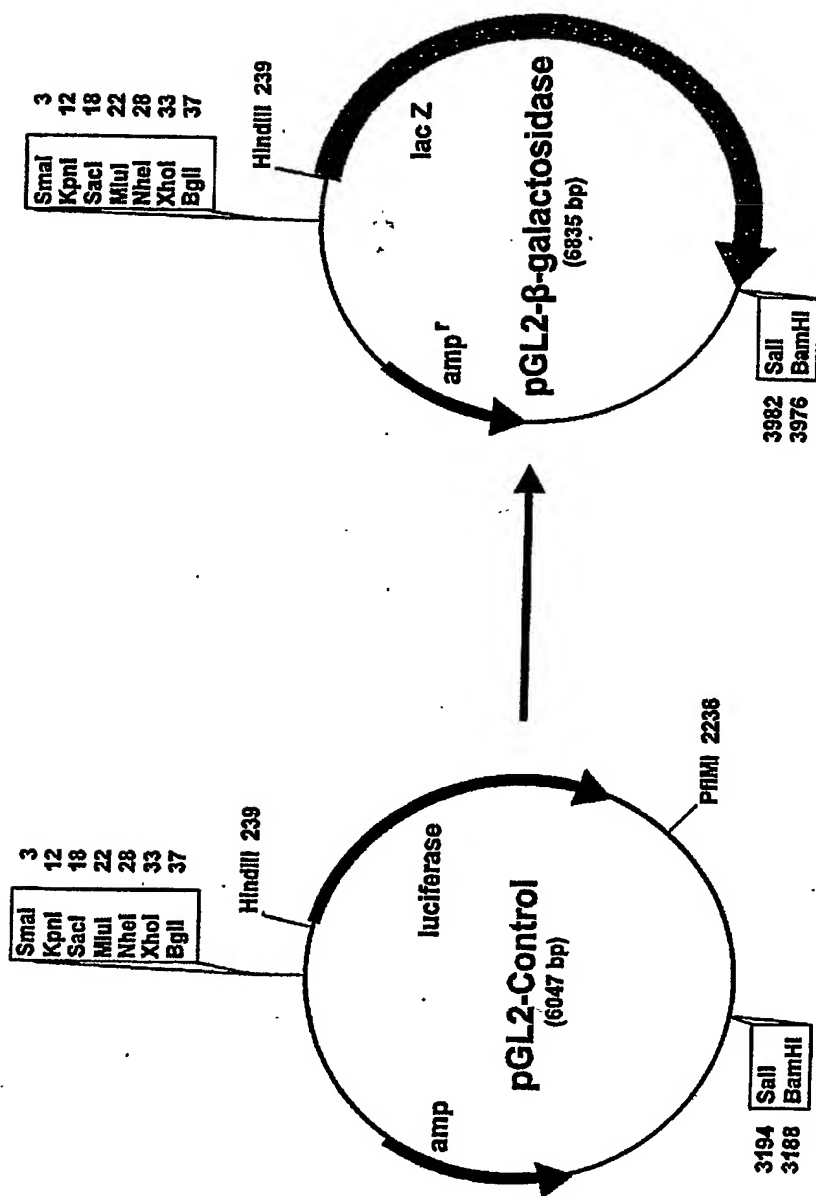


FIGURE 3 B

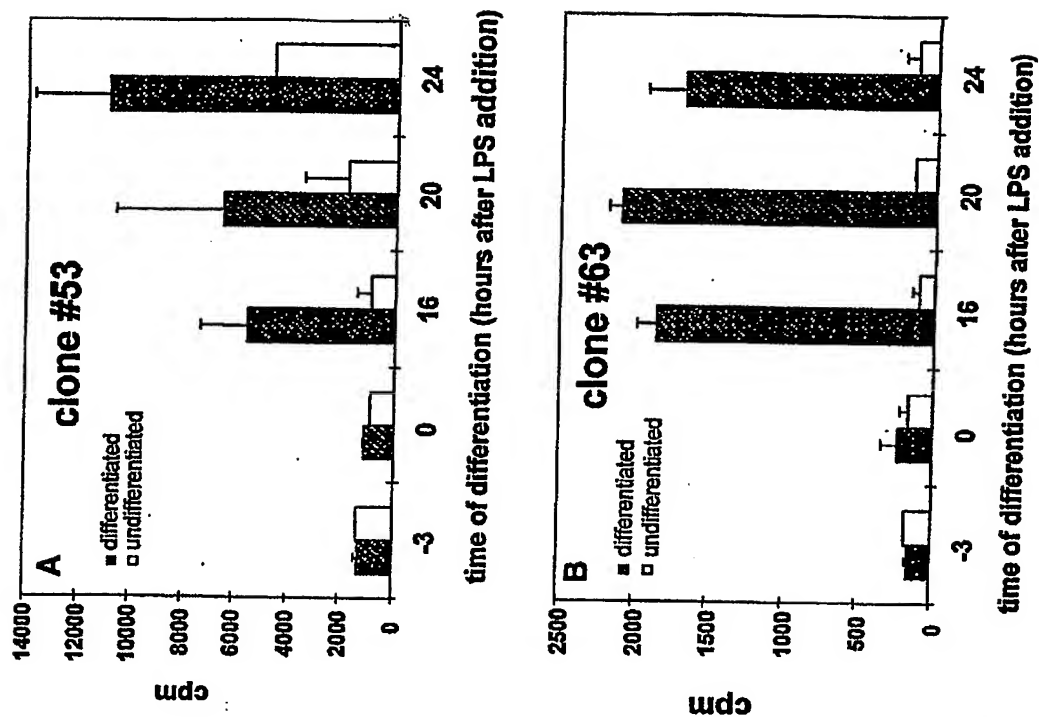


FIGURE 4

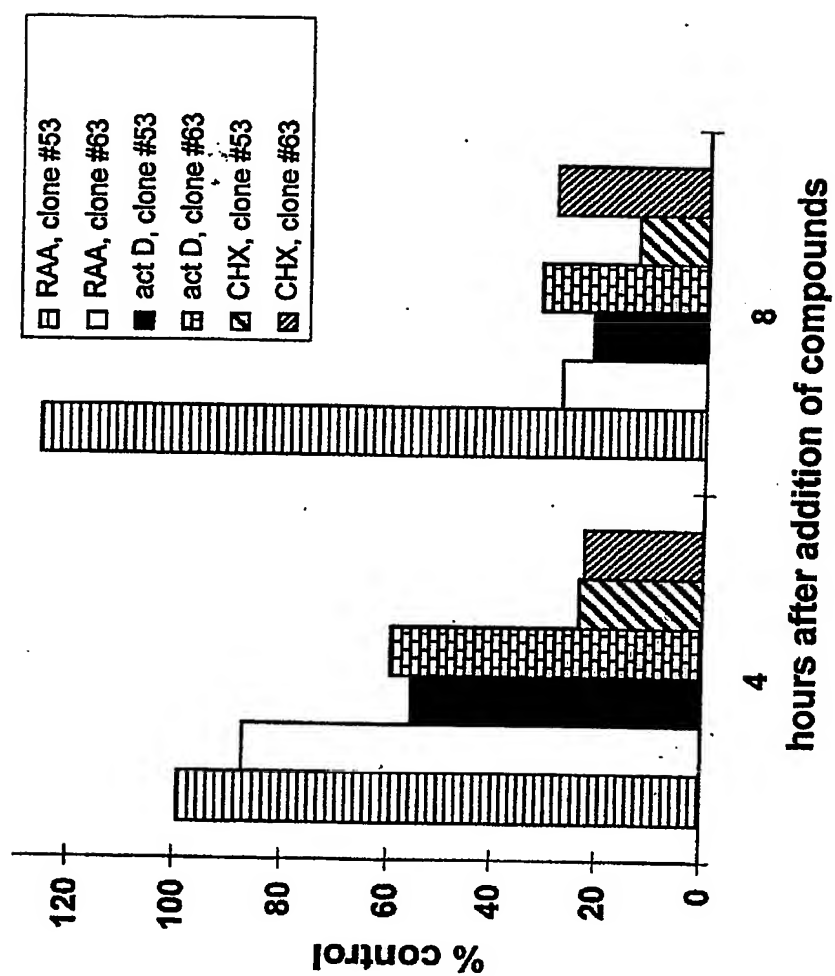


FIGURE 5

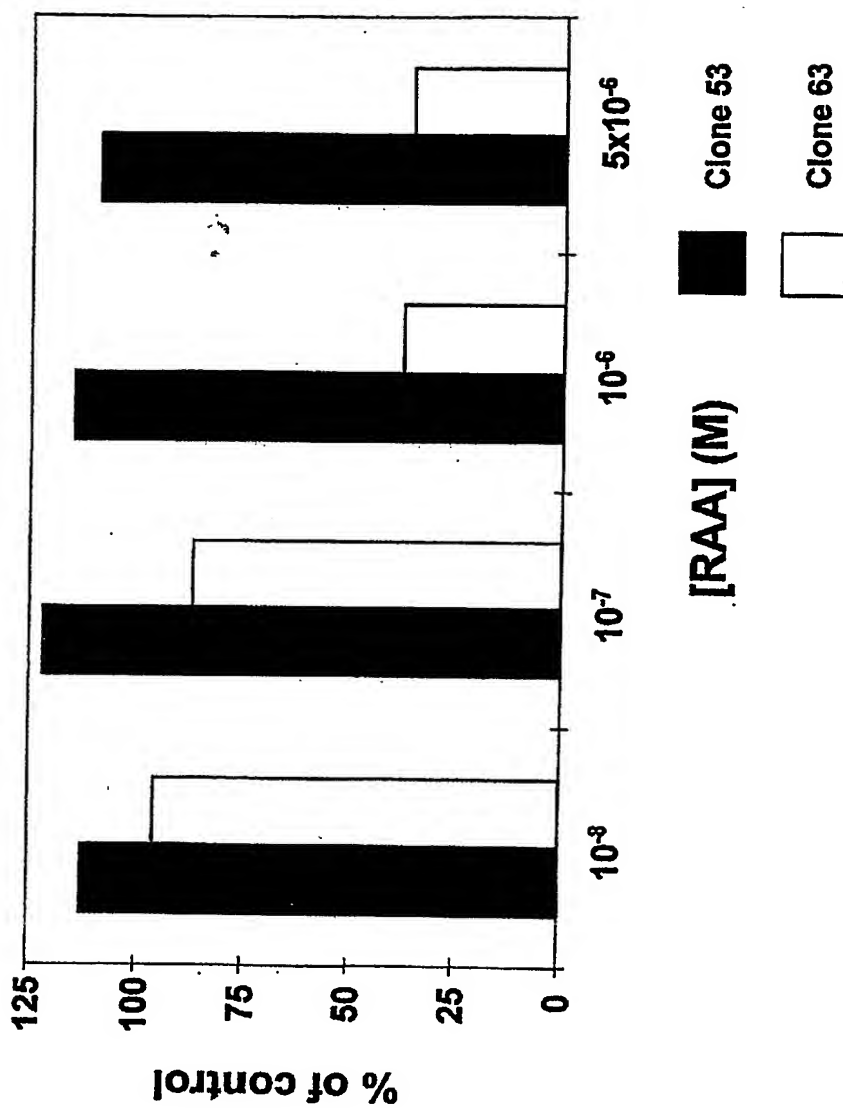


FIGURE 6

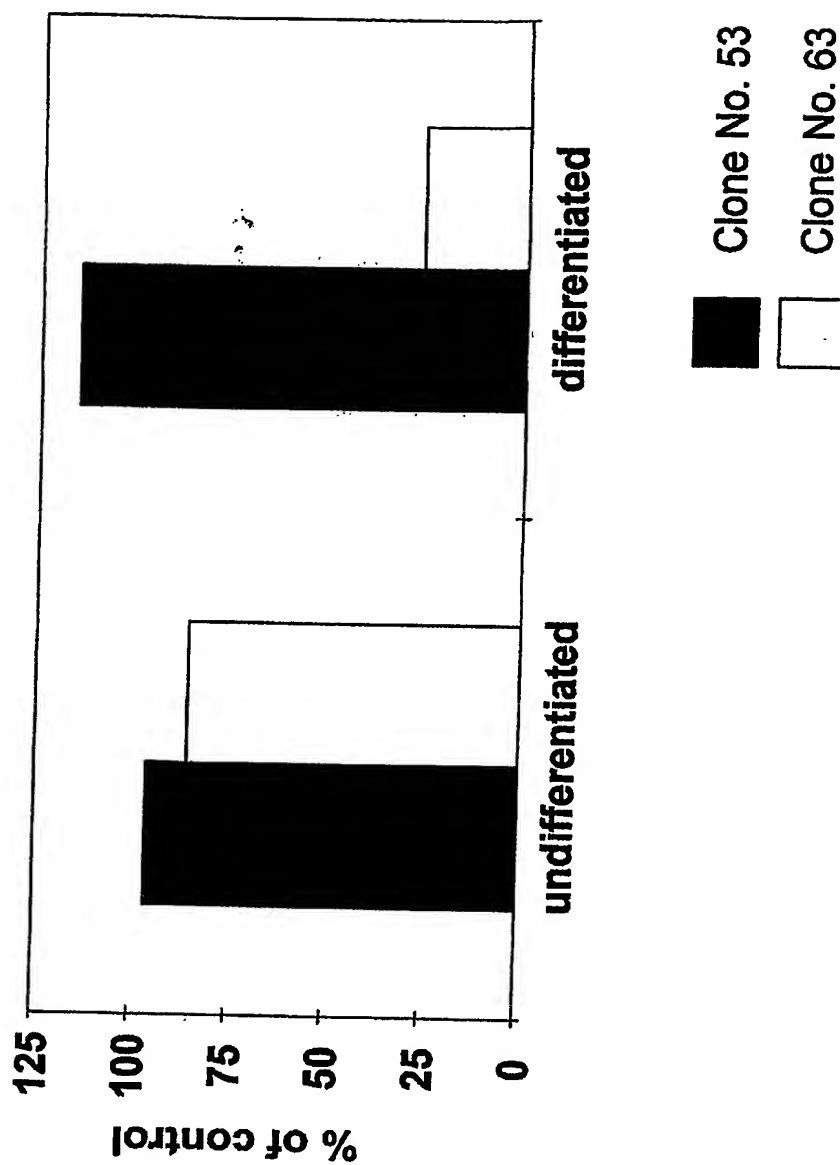


FIGURE 7



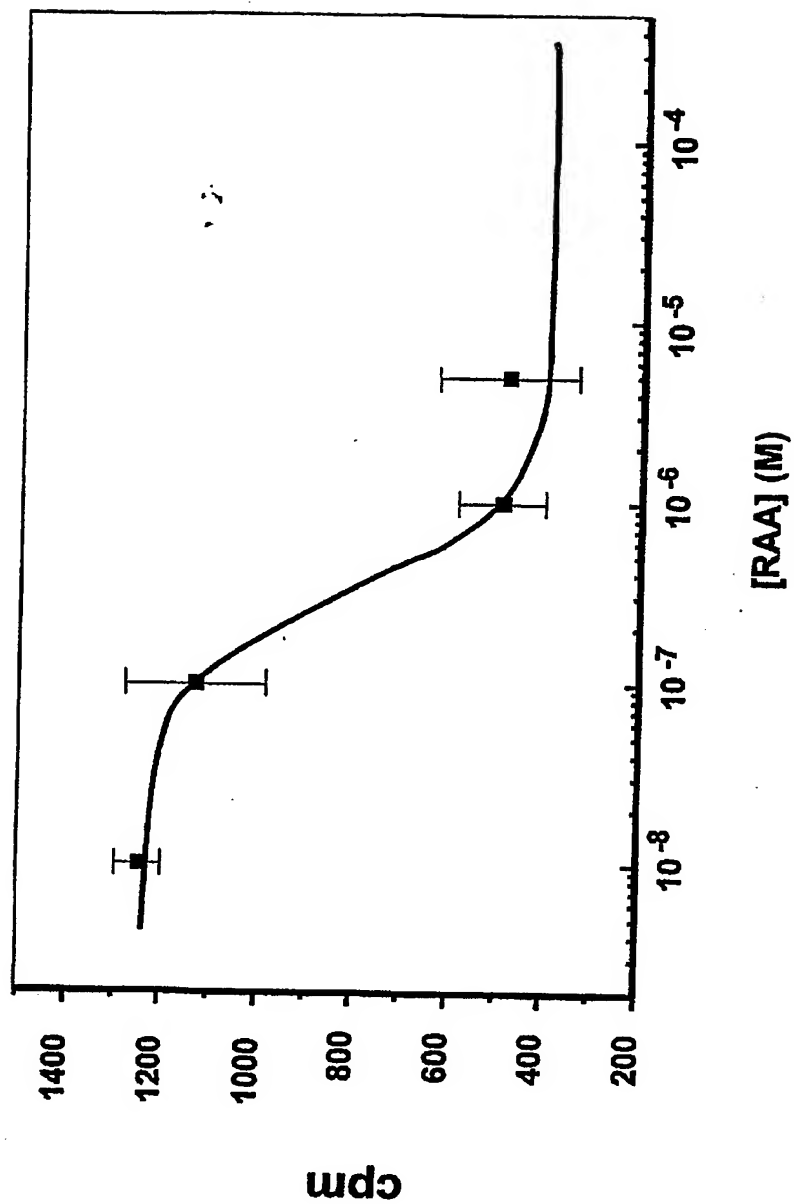


FIGURE 8


APP construct: 

■ AUUUA {Bold/Underline}  
 ★ potential polyA signal sequence {Bold/Italics}  
 Restriction Sites {Bold}

	<b>NotI</b>
1	GGGCGCCCA CAGCAGCCTC TGAAGTTGCA CAGCAAAACC ATTGCTTCAC TACCCATCGG TGTCATTTA TAGATAAAG TGGGAAGAA CAARCCCGTT
101	TTATGATTTA CTCATTATCG CCTTTTGACA GGTGTGCTGT AACACAGTA GATGCTGAA CTTEAATTA TCCACACATC AGTAATGTAT TCTATCTCTC
201	TTTACATTTT GGTCTCTATA CTCATTATT AATGGSTTT GTGTACTGTA AAGAAATAG CTGTATCAA CTAGTGCATG AATAGATTCT CTCCTGATTA
301	TTTATCAGAT AGCCCCCTTAG CCAGTTGTAT ATTATCTTG TGGTTTGTGA CCCAATTAAG TCCCTACTTA CATATGCTTT AAGAATCGAT GGGGGATGCT
401	TCATGTGAAC GTGGGAGTTC AGCTGCTTCT CTGCTTAAG TATCTCTTC CTGATCATA TGCTTTTAA AGTTAAACAT TTTTACTAT TTCAGATGCT
501	TTAGAGAGAT TTTTCTTCC ATGACTGCTAT TTTACTGTAC AGATTGCTGC TTCTCTATA TTTGTGAT AGGAATTAAG AGGTACACA CGTTTGTTC
601	TTGCTGCCCTG TTTTATGTC ACACATTAGG CATTGAGACT TCAAGCTTTT CTTTTTTGT CCACGTACT TTGGTCTTT GATAAAGAA AGATCCCTG
701	TTCAATTGTA GCACTTTAC GGGCGGGTG GGGAGGGTG CTCTGTGGT CTTCATTAC CAGAACTCT CCAAAACAT TTTCTGCAGG ATGATTGTAC
801	AGATCATTTG CTTATGACAT GATCGCTTTC TACCTGTAT TACATTAATA AATTAATAA AATACCCCG GGCAGACTT TTCTTTGAAG GATGACTACA
901	GACATTAAT AATCGAGTA ATTTTGGTG GGGAGAGAG GCAATTCAA TTTTCTTAA CCAGTCTGAA GTTTCATTTA TGATACAAA GAAGATGAAA
1001	ATGGAAGTGG CAAATTAAG GGATAGGAA GGCATGCCCTG GACAAACCT TCTTTTAGA TGTGCTTCA ATTGTATTA AATGGTGTTC TCATGTAGCG
1101	GCGGC <b>NotI</b>

FIGURE 9

Length: 1105 bp

stop codon {***Bold/Italics/Underline***}bcl-2 $\alpha$ -long construct: ■ AUUUA {***Bold/Underline***}Restriction Sites {**Bold**}

NotI

1 GCGCGCGCTG AGTCAACAT GCCTGCCCA AACAAATATG CAAAGGTTT ACTAAGCAG TAGAAATAT ATGCATGTG AGTGATGATC CATGAACAA

101 AGCTGCGGC TGTTTAAGA AATAATAC ACATATAAC ATCACACACA CACACACACA CAACATTA CACTCTTCAG GCAACAGTC

201 GATCAGCTA TTTACTGCCA AAGGGAATA TCATTATTT TTTACATAT TAAGAAAAA AGATTATTT ATTTAAGACA GTCCATCRA AACTCTGTC

301 TTTGGAATC CGACCACTAA TTGCCASCA CGCTTCGTG TGCCTCCACC TGAATCTCT GTGCCGTAA ACATAGATT GCTTTCCATG TTGTTGCCG

401 GATCACCATC TGAAGACAG ACGGATGGA AAGGACCTG ATCATTTGGG AAGCTGGCT TCTGGCTGCT GGAGCTGGG GAGAAGTGT TCATTCTCT

501 GCAATTTCTT GCGCTGGGG CTGTATATT MACAGAGGA GGGTTCTCT GGGGGGAAGT CCATGCCCTC CTGCCCTGAA GAAGGACTC TTTCATATG

601 ACTCACATGA TGCATACCTG GTGGGAGGA AAGAGTTGG AACTTCAGT GGACCTAGTA CCACCTGAGA TTTCCACGCC GAAGGACAG GATGGGA

701 ATGCCCTTAA ATCATAGGA ASTATTTTT TAAGCTACCA ATTGTCCGA GAAGACAT TTAGCAATTT ATCAATATC ATCCAGTACC TTAAGCCCTG

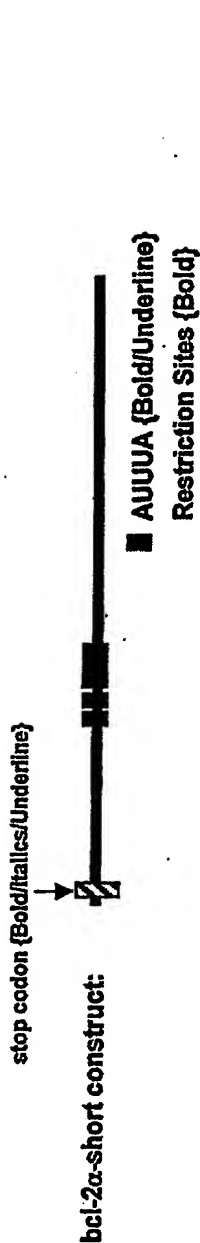
801 ATTGTGTATA TTCAATATT TTGGATACG ACCCCCCAAC TCCCAATCT GGTCTGTCT GAGTAAGAA CAGATCTCT TGGACTTGA GGAAGTGGG

901 CCGC

NotI

Length: 904 bp

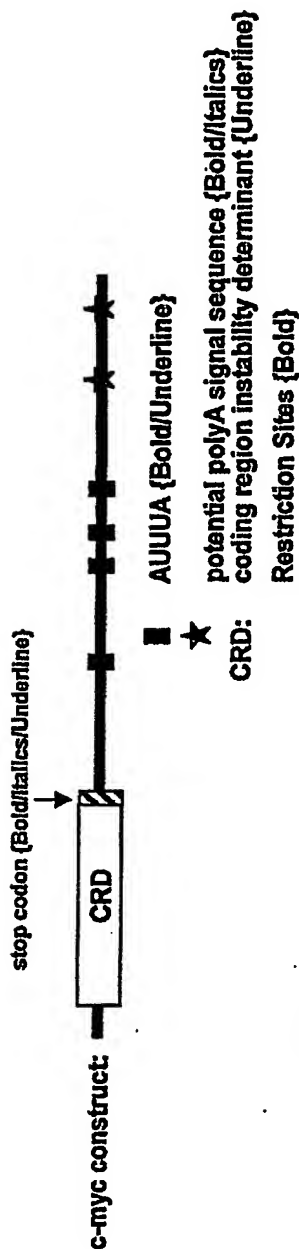
FIGURE 10



1	GCGGCCGCTG AAGTCAACAT GCCTGCCCA AACHAATATG CAAAGGTTT
51	ACTRAGCAG TAGAATAAT ATGCAATTGTC AGTGATGTAC CATGAACAA
101	AGCTGCAGC TGTTTAAGA AAATATACAC ACATATAAC ATCACAACA
151	CAGACAGCA CACACACACA CAACAATTAA CAGTCTCAG GCAAACGTC
201	GAATCAGCTA TTTACTGCCA AAGGGAATA TCATTATTT TTTACATTAT
251	TARGAATAA ACATTTATTT ATTATAGACA GTCCCATCAA AACTCCTGTC
301	TTTGGAAATC CGACCACTAA TTGCCAAGCA CCGCTTCGTG TGGCTCCACC
351	TGGATGTTCT GTGCCGTGTA ACATAGATTC GCTTTCATG TTGTTGGCGG
401	GATCACCATC TGAAGACAG ACGGTGGA AAAGGACCTG ATCATTTGGG
451	AAGCTGGCTT TCTGGCTGCT GGAGGCTGG GAGAAGGTGT TCATTCACTT
501	GCATTTCCTT GCCCTGGGG CTGTGATTT AACAGAGGA GGGTTCCTGT
551	GGGGGAGT CCATGCCCTCC CTGGCCTGAA GAAGACTC TTTCATATG
601	ACTCACATGA TGCATACCTG GTGGGAGGA AAGAGTTGG AACTTCAGAT
651	GGACCTAGTA CCACTGAGA TTTCCACCCC GAAGGACGC GATGGGAAA
701	ATGGGCCCC

NotI

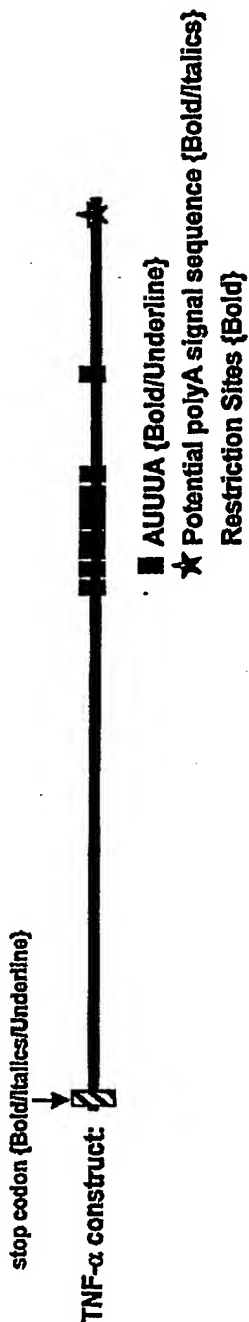
FIGURE 11



1	CGCGCCGCTC	GGAGCTTTT	TGCCCTGGT	GACGATCC	CGGAGTTGGA
51	AAACAATGAA	AGGCCCCCA	AGGTAGTTAT	CCTTAATAAA	GCCACAGCAT
101	ACATCCTGTC	CGTCCRAGCA	GAGGAGCAA	AGCTCATTTC	TGAAGAGGAC
151	TTGTTCGCGA	AACGACGAGA	ACAGTTGAAA	CACAACTTG	AACAGCTACG
201	GAATCTTGT	GCGTAGGAA	AGSTAAGGA	AACGATTCCT	TCTGCACGAA
251	ATGTCCTGAG	CAATCACCTA	TGAATTTGTT	TCAATGCAAT	GATCAAAATGC
301	AACCTCACAA	CCTTGGCTGA	GTCTTGAGAC	TGAAGATTI	AGCCATTAAG
351	TAACTGCCT	CAATTTGGAC	TTTGGGCATA	AAAGAACTTT	TTTATGCTTA
401	CCATCTTTT	TTTTTCCTTA	ACAGATTGTT	ATTAGAAT	TGTTTTTAAA
451	AAATTTTAA	ATTACACAA	TGTTCTCTG	TAAATATTGC	CATTAAATGT
501	AATAAATTT	AATAAAGCT	TTATAGCAGT	TACACAGAAT	TTCAATCCTA
551	GTATATAGTA	CCTAGTANTA	TAGTACTAT	AAACCTAAT	TTTTTTTATT
601	TAACTACATT	TGCTTTTAA	AGTTGATTT	TTTTCATTG	TTTTTAGAAA
651	AAATAAATA	ACTGGCAAT	ATATCAATGA	GCCATAG	

Length: 688 bp

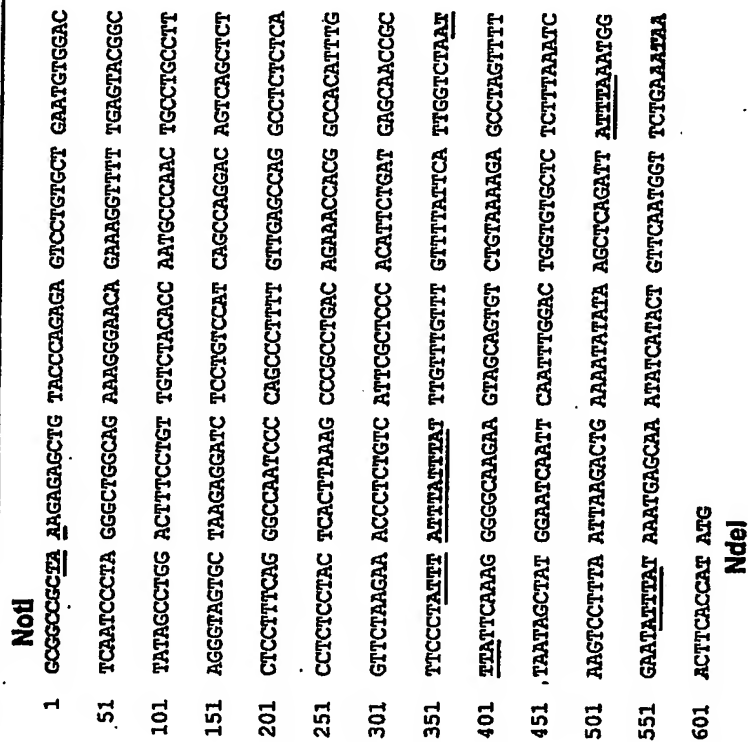
FIGURE 12



NotI	
1	GGGGGGCTG AGGAGGAGCA ACATCCAAAC TTCCCAACG CCTCCCTGC CCCATCCCT
61	TTATTACCC CTCCTTCAGA CACCTTCAC CTCCTTCGG TCBAAGAGG AATTGGGGC
121	TTAGGTGG AACCAAGCT TAGACTTTA AGCAACAGA CCACCCTTC GAACCTGGG
181	ATTCAGGAT GTGTGGCTG CACGTGAAG TGCTGGCAC CACTAAGAT TCBAACCTGGG
241	GCCTCAGAA CTCACGGGG CCTACAGCTT TGATCCCTGA CATCTGGAT CTGGAGACCA
301	GGGAGCTTT GGTCTGACC AGAAGCTGC AGGACTGAG AAGACTCAC CTAGAAATTG
361	ACACAGTGG ACCTTAGGCC TTCTCTCTC CAGATGTTT CAGACTTCT TCGACACGG
421	AGCCAGCCC TCCCATGGA GCCAGTCC TCTATTATG TTGCACTTG TGATTATTTA
481	TTATTATTT ATTATTATT TATTACAGA TGAATGATT TATTGGGAG ACCGGGTAT
541	CCTGGGGAC CCATGTAGG AGCTGCTTG GCTCAGACAT GTTTCGGTG AAACGGAGC
601	TGAACAATAG GCTGTCCCA TGTAGCCC TGSCCTCTGT GCCTCTTTT GATTATGTT
661	TTTAAATAT TTATCTGATT AAGTTGCTA AACATGCTG ATTGGTGAC CACTGTAC
721	TCATTGCTGA GCCTCTGCTC CCCAGGGAG TTGTGTCTGT AATGCCCTA CTATTCAGTG
781	GCGAGAAATA AAGTTGCTT CATATG
NdeI	

Length: 806 bp

FIGURE 13



## FIGURE 14

VEGF construct: 

- AUUUA {Bold/Underline}  
 ★ Potential polyA signal sequence {Bold/italics}  
 Restriction Sites {Bold}

	<b>NotI</b>
1	GGGCGCCCAT TGCCTGTGCTT TGGGGATTC CTCACATGC TGCACGGCA TCTGCCCCC AGGGGACTG CTGGAGAT TCAGAGCCT GGGCGGCCTT
101	CGCTTACTCT CACCTGCTTC TGAGTTGCC AGGAGGCCAC TGGCAGTGT CCGGGCGAAG AGAAGAGCA CATGTGTTGA AGAAGCAGCC CATGACAGCT
201	CCCCCTCCTG GGACTCGCC TCACTCTCTT CCTGCTCCCC TTCTGSGGT GAGCCTTAA AGGACCTATG TCCTCACACC ATTGAAACCA CTAGTTCTGT
301	CCCCCCAGGA GACCTGGTTG TGTGTGTG AGTGGTTGAC CTTCCTCCAT CCGCTGGTCC TTCCCTTCCC TTCCCGAGGC ACAGAGAGAC AGGGCAGGAT
401	CCACGTGCC ATTGTGGAG CAGAGAAAG AGAAGTCTT TTATATACG TACTTATTA ATATCCCTTT TTAATTAGAA ATTAAACAG TTAATTAAAT
501	TAAAGAGTAG GGTITTTTTT CAGTATCTT GGTAAATTT TAAATTCAC TATTATGAG ATGTATCTTT TGTCTCTCTT TGTCTCTCTA TTGTACCGG
601	TTTTTGTATA TAAATTCAT GTTCCAATC TCTCTCTCCC TGTGCGTGA CAGTCACTAG CTTATCTTGA ACAGATATTT AATTTGCTA ACACTCAGCT
701	CTGCCCTCCC CGATCCCTTG GCTCCCGAGC ACACATTCCT TTGAATNAG GTTCAATAT ACATCTACAT ACTATATATA TATATTTGSC AACTTGTATT
801	TGTGTGTATA TATATATATA TATGTTTNG TATATATG AGTCTGATTA AATAGACATT GCTATCTCTG TTTTATATAG TAAATACAAA ACAAGAAAAA
901	ATAGAGAAAT CTACATACTA AATCTCTCTC CTTTTTAAAT TTTATATTT GTTATCATTT ATTATTTGCT GCTACGTGTT ATCGTATAA ATTGTGGGA
1001	AAAGATATTA ACATCAGTC TTGTCTCTA GTGACGTTTT TCGACATAT CCGTACTACA TATTATTTT TAAACAAGA CAAGAATAA CAGACATAT
1101	<b>G</b>
	<b>NdeI</b>

Length: 1101 bp

FIGURE 15



VEGF 3'UTR hypoxia domain construct: 

■ AUUUA {Bold/Underline}  
Restriction Sites {Bold}

NotI	
1	GCGGCCGCAT TCCTGTAGAC ACACCCACCC ACATACATAC <u>ATTTATATAT</u>
51	ATATATATTA TATATATATA AAAATAAATA TCTCTATTTT ATATATATAA
101	AAATATATATA TTCTTTTTT AAATTAACAG TGCTAATGTT ATTGGTGTCT
151	TCACITGGATG AACATATG
NdeI	

Length: 168 bp

FIGURE 16

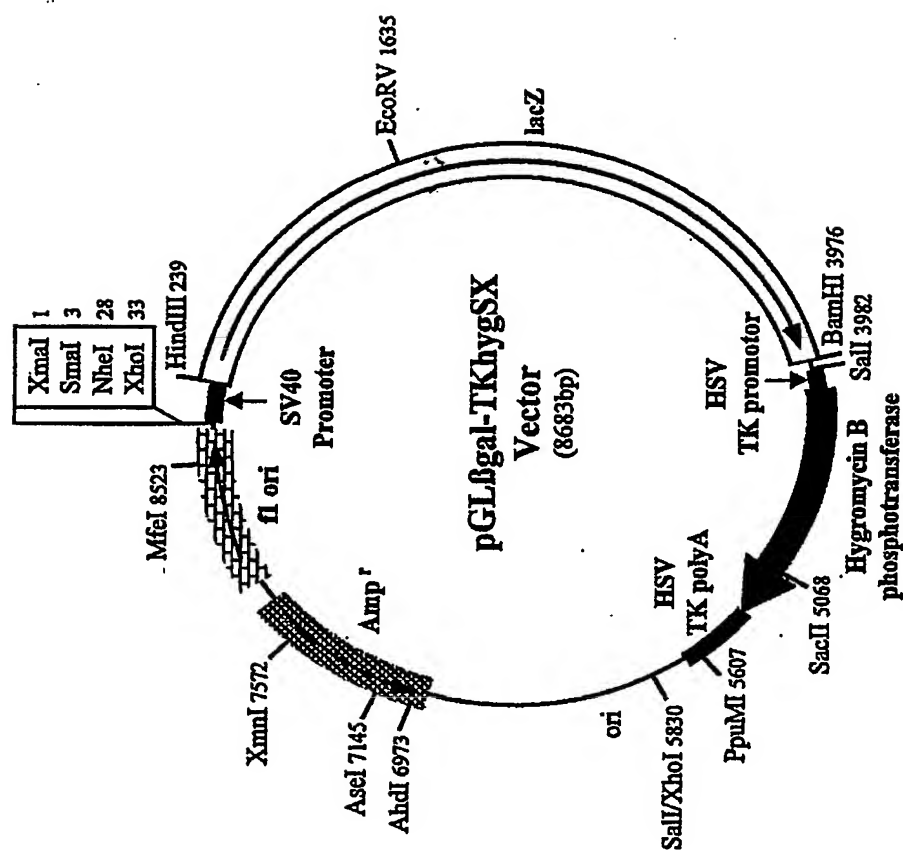


FIGURE 17

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